

10045180-01000

XY-1 AP-1
SAA1 --TAGATATG AACTCAGAGG GACTTCATTT CAGAGGCATC TGCCATGTGG³⁹¹
SAA2 TTTAGACATG AACTCACAGG GATTTCACT- CAGGGTCATC TGCCATGTGG³⁹⁷

AP-2 NEIL-6/XY-1
SAA1 CCCAGCAGAG CCCATCCTGA GGAAATGACT GGTAGAGTCA GGAGCTGGCT³⁴¹
SAA2 CCCAGCAGGG CQCATCCTGA GGAAATGACC GGTATAGTCA GGAGCTGGCT³⁴⁷

YY-1
SAA1 TCAAAGCTGC CCTCACTTCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA²⁹¹
SAA2 GAAGAGCTGC CCTCACTCCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA²⁹⁷
* *****
NFKB AP-2 SAE
SAA1 CGGGGCTCCC ACTCTCAACT CCGCAGCCTC AGCCCCCTCA ATGCTGAGGA²⁴¹
SAA2 CGGGGCTCCC ACTGGCATCT CTGCAGCTGC ACTTCCCCCA ATGCTGAGGA²⁴⁷

-240
SAA1 GCAGAGCTGG TCTCCTGCCC TGACAGCTGC CA-GGCACA- -----TC²⁰¹
SAA2 GCAGAGCTGA TCTAGACCCC TGTCCATTGC CAAGGCACAG CAAACCTCTC¹⁹⁷

-200 GRE NEIL-6/STAT AP-1.....
SAA1 TTGTTCCCTC AGGTTGCACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC¹⁵¹
SAA2 TTGTTCCCAT AGGTTACACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC¹⁴⁷

-150 YY-1
SAA1 CACTGGCATC CAGGAAGTTG TCTTAGACCG TTTTGTAGGG GAAATGACCT¹⁰¹
SAA2 CACCGGCATC CAGGAAGTTG TCTTAGACCA GTTTGTAGGG GAAATGACCT⁹⁷
*** *****
-100 NFKB
SAA1 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTCTTCC CTCCAAGAA⁵¹
SAA2 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTCTTCC CTCCAAGAG⁴⁷

-50 SP-1
SAA1 ACCAGCAGGG AAGGCTCACT ATAAATAGCA GCCACCGCTC CCTGGCAGGC¹
SAA2 ACCAGCA--- -AGGCTCACT ATAAATAGCA GCCACCTCTC CCTGGCAGAC¹

FIG. 1

202210-09541001

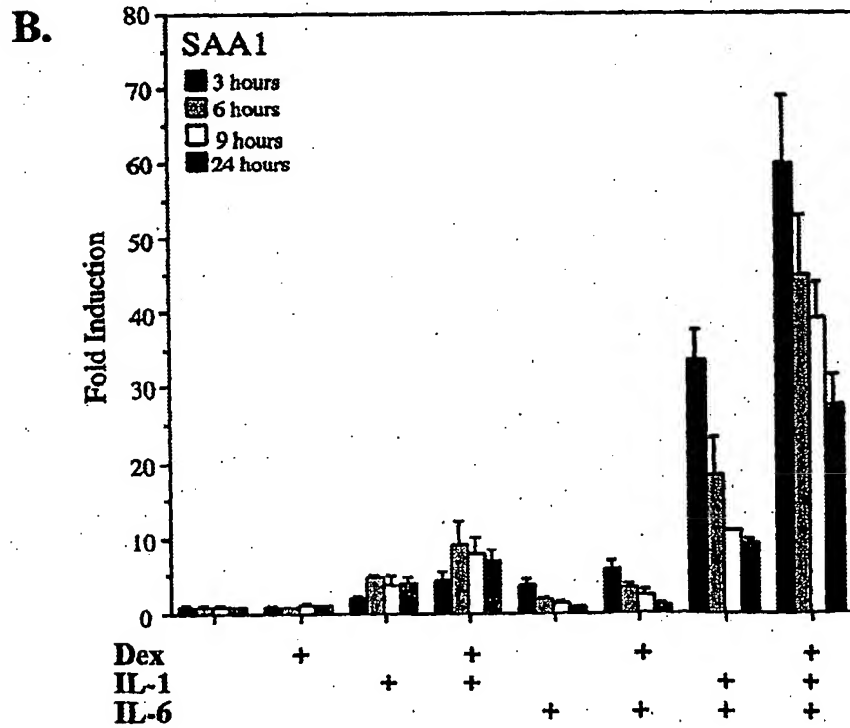
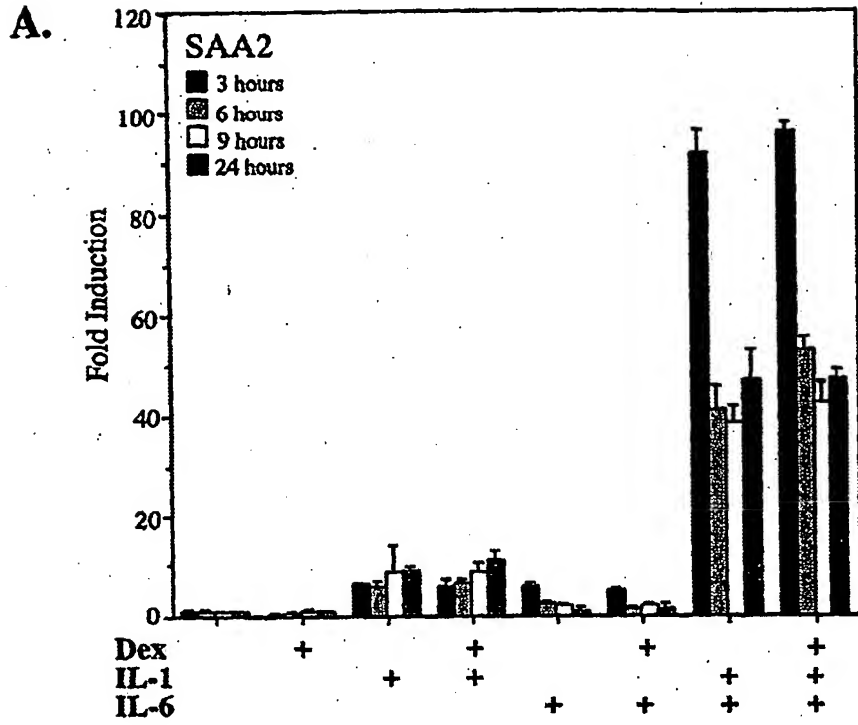


FIG. 2

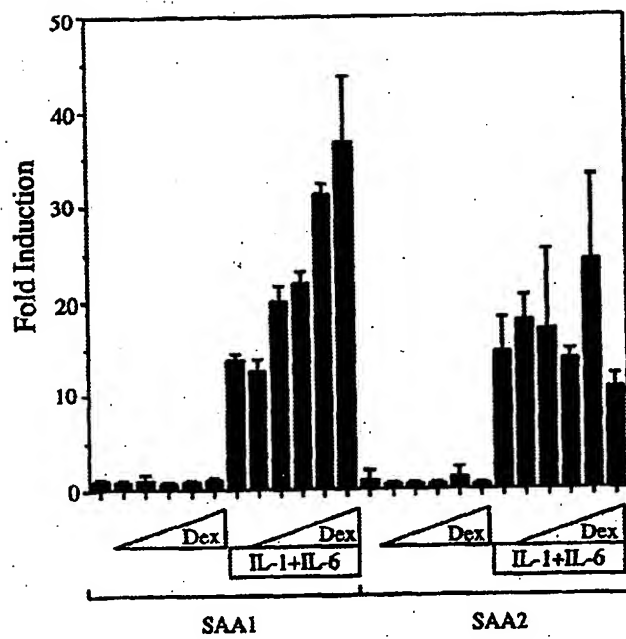


FIG. 3

10045360-012202

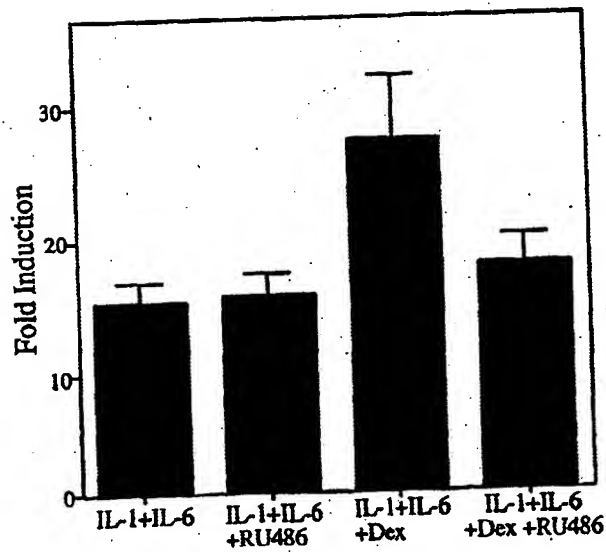


FIG. 4

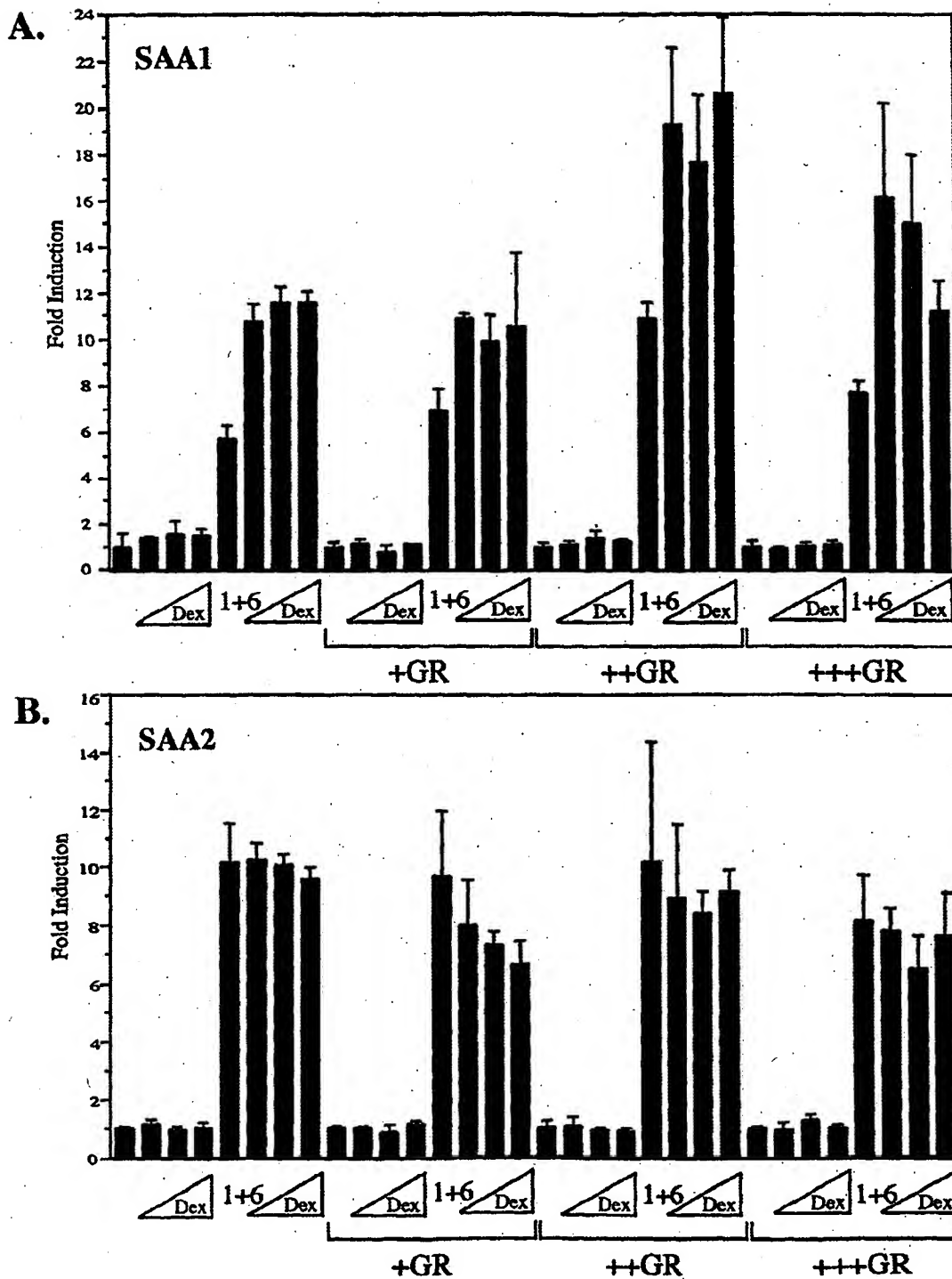


FIG. 5

10045360.012202

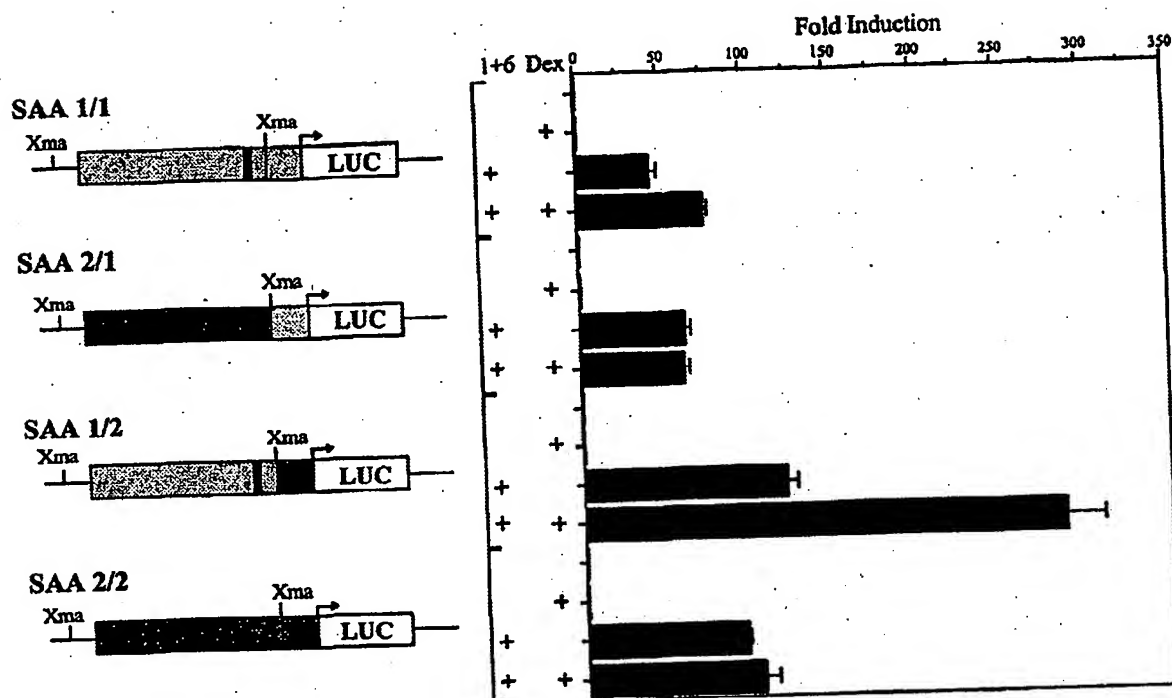


FIG. 6

A.

SAA1	CA- <u>GGCACA</u> -----TCTTGTTCCCTCAGGTTGCACA
GREI	CA-GGCACAGCAAACCTCTCTTGTTCCCTCAGGTTGCACA
GRE	CAAGGCACA-----TCTTGTTCCCATAGGTTACACA
SAA2	CAAGGCACAGCAAACCTCTCTTGTTCCCATAGGTTACACA
Consensus	GGTACA NNNTGTTCT
GRE	

B.

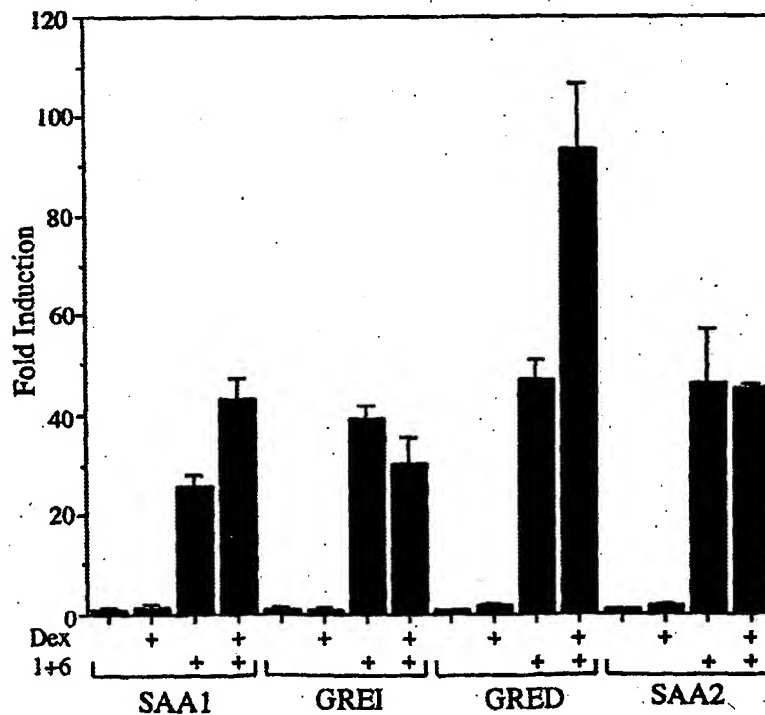


FIG. 7

202210-09254004

A.

SAA1 CAGACAAATACCTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG²⁴⁶
SAA2 CAGACAAATACCTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG²⁴⁶

 exon3 exon4

SAA1 TCTGGGCTGCAGAAGCGATCAG|CGATG—//—//—TGAGCTTCCTCTTCACTCTGCTC⁴²⁶
SAA2 CCTGGGCCGCAGAAGTGATCAG|CAATG—//—//—TGAGCTTCCTCTTCACTCTGCTC⁴²⁶

SAA1 TCAGGAGATCTGGCTGTGAGGC-TCAGGGCAGGGATACAAAGC----GGGG-----⁴⁷²
SAA2 TCAGGAGACCTGGCTATGAGCCCTCGGGGCAGGGATTCAAAGTTAGTGAGGTCTATGTCC⁴⁸⁶

SAA1 AGAG-----GGTACCAATGGGTATCTAATAAATACCTAAGAGGTGGAAAAA⁵²⁰
SAA2 AGAGAAGCTGAGATATGGCATATAATAGGCATCTAATAAATGCTTAAGAGGTGGAAAAA⁵⁴⁶

B.

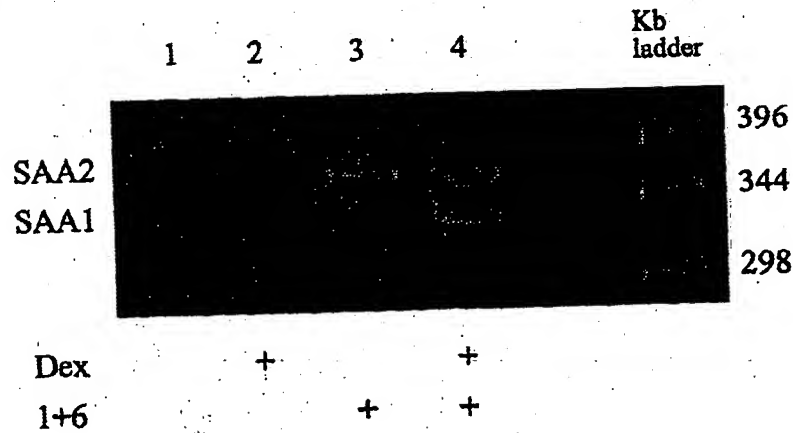


FIG. 8